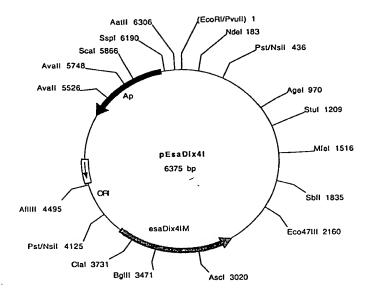
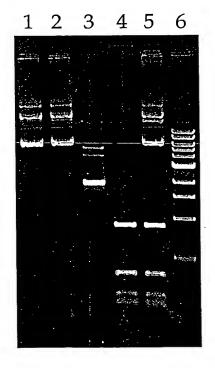


Fig. 1



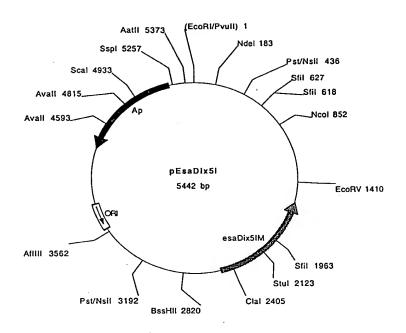
B.

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Figd

A



В.

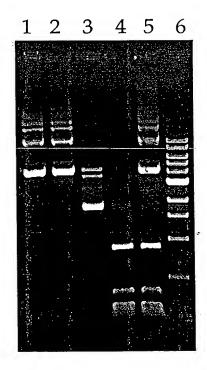


Fig. 3.

Me IM

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Fig. 4.

SEQ.10 NO2

PSQ DIX 4IM

1 ATGCCTACACTGGATTGGCCCGGTAAACAGTTAAGCTTCCCACCA SFQ ID M P T L D W P G K Q L S F P P 46 GCTACCTCCTTGCATCTGGAGAGTGTGGTCACTGAGGGAGCGGAG ATSLHLESVVTEGAE 91 TCACCGCCTAATCGTCTGATTTGGGCGGACAACCTGCCGCTAATG S P P N R L I W A D N L P L M 136 GTAGATTTGTTGGCCGAATATGAAGGGAAAATCGATCTGATCTAC V D L L A E Y E G K I D L I Y 181 GCCGATCCCCTTTTTTTACGGATCGTACTTATGCGGCGCGAATT ADPFFTDRTYAARI 226 GGTCATGGGGAGGATTCGCGTCGTCCACAAACCTGGCAGCTTGCA G H G E D S R R P Q T W Q L A 271 GAAGGATATACGGACGAGTGGAAGGATTTAGATGAATACCTGGAC E G Y T D E W K D L D E Y L D 316 TTCCTTTATCCACGCCTGGTACTGATGTATCGACTGCTGGCACCA F L Y P R L V L M Y R L L A P 361 CACGGAACGCTCTACTTGCACCTGGACTGGCACGCCAATGCCTAC H G T L Y L H L D W H A N A Y 406 GTACGTGTACTGCTTGATGAGATCTTCGGGCGACAGCGGTTTCTC V R V L L D E I F G R Q R F L 451 AACGAGATCGTCTGGATCTATCACGGCCCCTCAGCCATCCGACGC NEIVWIYHGPSAIRR 496 GCCTTCAAGCGCAAACATGATACCATCTTGGTTTATGTGAAAGGT AFKRKHDTILVYVKG 541 GAAAACTATACATTCAATGCGGATGCGGTTCGTCAACCTTACCAT E N Y T F N A D A V R Q P Y H 586 CCGAGCACNCATAAGACCTTCGCTTCCTCCCCGAAGGCCGGCTTT P S T H K T F A S S P K A G F 631 GGTAAGGTGCCGGATCTGCAGCGCGGCAAAGTGCCCGAAGACTGG G K V P D L Q R G K V P E D W 676 TGGTATTTTCCGGTCGTGGCCCGTCTACACCGAGAACGGAGCGGC W Y F P V V A R L H R E R S G 721 TATCCGACTCAAAAGCCTCAAGCCTTGCTGGAGCGGATCCTGCTG Y P T Q K P Q A L L E R I L L 766 GCCTCCTCGAACGCAGGCGATCTGGTGGCAGACTTCTTCTGCGGC A S S N A G D L V A D F F C G 811 TCAGGGACAACCGCTGTGGTGGCAGCCCGTCTGGGACGGCGCTTC S G T T A V V A A R L G R R F 856 CTGGTCAACGATGCAAGCTGGCGCGCCGTTCATGTGACACGCACA LVNDASWRAVHVTRT 901 CGCTTGCTACGCGAGGGAGTAAGTTTCACTTTTGAACGCCAGGAA R L L R E G V S F T F E R Q E 946 ACTTTACTCTACCTATCCAGCCACTTCCACCAGATTGGTTGATC T F T L P I Q P L P P D W L I 991 ATCGCCGAGGAGCAGATTCGCCTCCAAGCACCCTTTCTCGTAGAT I A E E Q I R L Q A P F L V D 1036 TTTTGGGAAGTGGACGATCAATGGGATGGCAAAATCTTCCGCAGC F W E V D D O W D G K I F R S 1081 CGTCATCAAGGCTTACGCTCCCGCCTTCAGGAGCAGGCGCCGCTC R H Q G L R S R L Q E Q A P L 1126 TCTCTACCATTGACCGGGAATGGACTGTTGTGTGTACGGGTAGTG S L P L T G N G L L C V R V V 1171 AGCCGTGAAGGGGAATACTATGAGTTCACAGGTCGAGCCGATAGC SREGEYYEFTGRADS 1216 CCTCACCCCGTATCGTTTTGA 1236 P H P V S F *

SERIA NO4

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1 ATGATCACGAACCTGATGGAAAACGATGTCATTGGCAAAATCTAC \SFQ(\alpha: \Sigma MITNLMENDVIGKIY SFQ (12:6 46 TTTGCCGACAACATGGAAGTCCTGCGAGGGCTTCCGGCGGCGTCC F A D N M E V L R G L P A A S 91 GTGGACCTGATCTACATCGATCCTCCGTTCAACACCGGAAAGGTT V D L I Y I D P P F N T G K V 136 CAGGAGCGCACTCAGCTCAAAACGGTGCGCTCCGAGTGGGGCGAT QERTQLKTVRSEWGD 181 CGCGTCGGATTCCAGGGCCGTCGCTACGAAAGCATCGTCGTGGGT RVGFQGRRYESIVVG 226 AAGAAGCGCTTTACCGACTTCTTCGACGACTATCTGGCTTTCCTG K K R F T D F F D D Y L A F L 271 GAACCGCGCCTGGTCGAAGCCCATCGTGTTCTGGCGCCCGCACGGG E P R L V E A H R V L A P H G 316 TGCCTCTACTTTCACGTCGACTACCGCGAGGTGCACTACTGTAAG C L Y F H V D Y R E V H Y C K 361 GTCCTTCTTGACGGCATCTTCGGTCGCGAGGCCTTTCTCAACGAG V L L D G I F G R E A F L N E 406 ATCATCTGGGCCTACGATTACGGCGGGCGTCCGAAGGACAGGTGG I I W A Y D Y G G R P K D R W 451 CCTCCTAAGCACGACAACATCCTGCTCTACGCCAAGACTCCCGGT PPKHDNILLYAKTP 496 CGCCACGTGTTCAATGCGGACGAAATCGAGCGCATTCCCTACATG RHVFNADEIERIPYM 541 GCTCCGGGCCTGGTTGGCCCCGAAAAGGCAGCCCGTGGAAAACTG APGLVGPEKAARGKL 586 CCAACCGACACGTGGTGGCATACGATCGTTCCGACCAGCGGCTCC P T D T W W H T I V P T S G S 631 GAGAAGACCGGGTATCCAACCCAGAAACCTTTAGGGATTCTCCGC E K T G Y P T Q K P L G I L R 676 CGTATTGTGCAGGCATCGTCTCATCCGGGGGCAGTCGTGCTCGAC RIVOASSHPGAVVLD 721 TTCTTCGCCGGCAGTGGGACAACAGGGGTAGCGGCTTTTGAGTTG F F A G S G T T G V A A F E L 766 GGCCGGCGTTTCATTCTGGTCGATAACCATCCGGAGGCCCTCCAG G R R F I L V D N H P E A L Q 811 GTGATGGCCAGGCGCTTCGACGGCATCGAGGGGATCGAATGGGTG V M A R R F D G I E G I E W V 856 GGCTTCGATCCGACACCGTACCAGAAGGGCGCAAAGCAGCGCCGC G F D P T P Y Q K G A K Q R R 901 TCCTGCCCGGCGCCCACCGGGTAA 924 SCPAPTG *

Fig.6.

nucia

1 GTGACCCACGAACCGACGGATGATCCCGATTTCATAGTGATGGCC S $\stackrel{\mathcal{E}}{-}$ $\stackrel{\mathcal{Q}}{-}$ M T H E P T D D P D F I V M A SFQ ſΔ 46 GCGAGCGCGGCGAACCTCGCTGATCGGTACGTAGCGAGTGAAGAC A S A A N L A D R Y V A S E D 91 GACCCTGGGTCGGCAGCCCGTTCGAGTGGATCCTTCGCGTTCCA D P W V G S P F E W I L R V P 136 TCCAGAACGAAGGCCGCGGTCGGTGAGCTGCTCGTGAGCGAATGG S R T K G A V G E L L V S E W 181 GCTAATGCCAAAGGCCTCCGTGTGAAGAGGTCGGGGTCCAGCGAT ANAKGLRVKRSGSSD 226 GCGGACCGCGTGATCAACGGGCATCGCATCGAGATCAAGATGTCG ADRVINGHRIEIKMS 271 ACTTTGTGGAAGTCCGGCGGCTTCAAGTTTCAGCAGATCCGGGAT TLWKSGGFKFQQIRD 316 CAGGAGTACGACTTTTGCCTCTGCCTTGGGATCAGCCCGTTCGAA Q E Y D F C L C L G I S P F E 361 GTGCACGCGTGGCTGCCCAAAGACCTATTGCTTGAGTACGTG V H A W L L P K D L L L E Y V I G H M G Q H T G A S G S D T 451 GCGTGGCTGGGGTTCCCAGCGGACGAGCCGTATGACTGGATGCGC AWLGFPADEPYDWMR 496 CCTTTCGGAGGTCGCTTAGGTCACGTCGAAGATCTCCTCCTCGCG P F G G R L G H V E D L L A 541 GCCGGCCCCGGTCCCTACTGA 561 AGPGPY

Fig. 7.

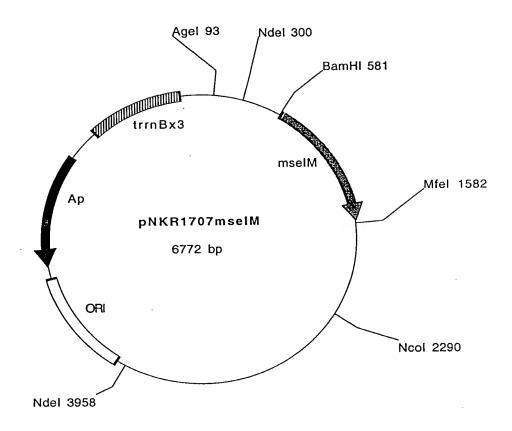
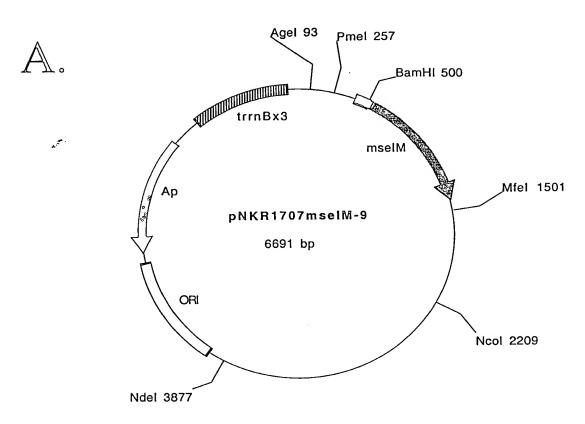


Fig. 8







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AgeI

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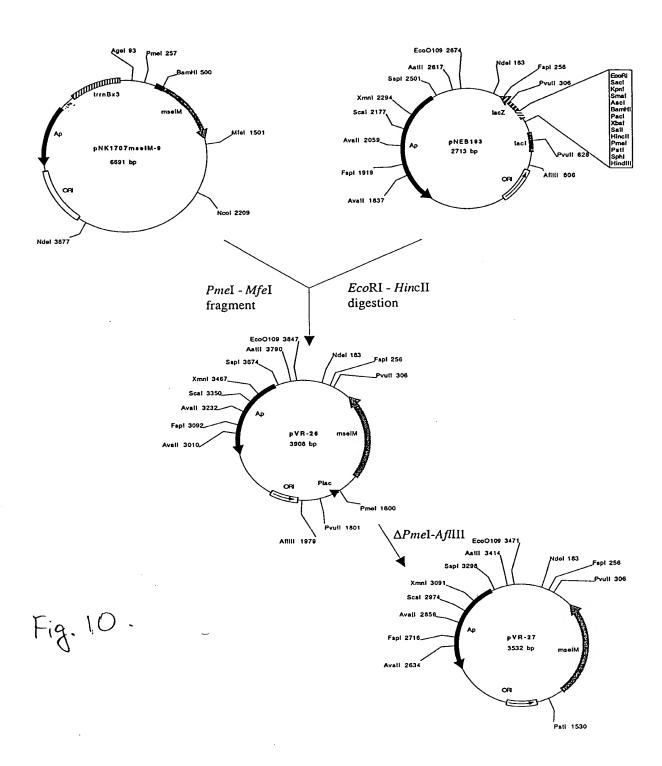
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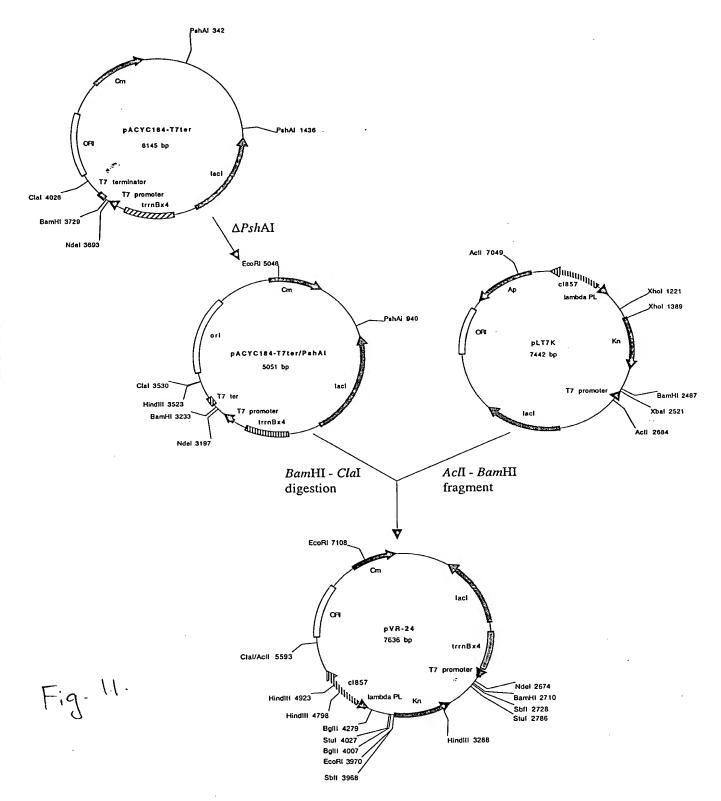
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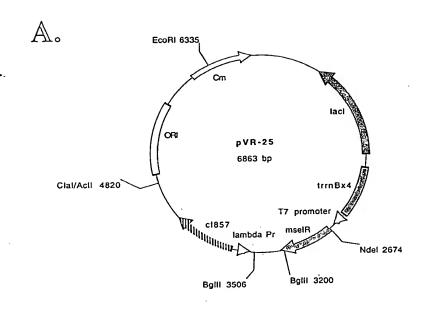
Bamhi
TGGATCC

Fig. 9.

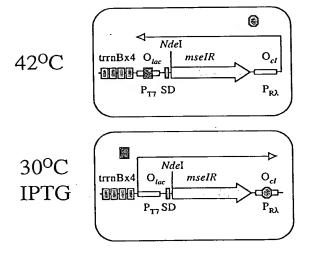
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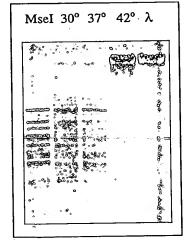






 \mathbb{B} .





LacI
CI₈₅₇

Fig. 12.

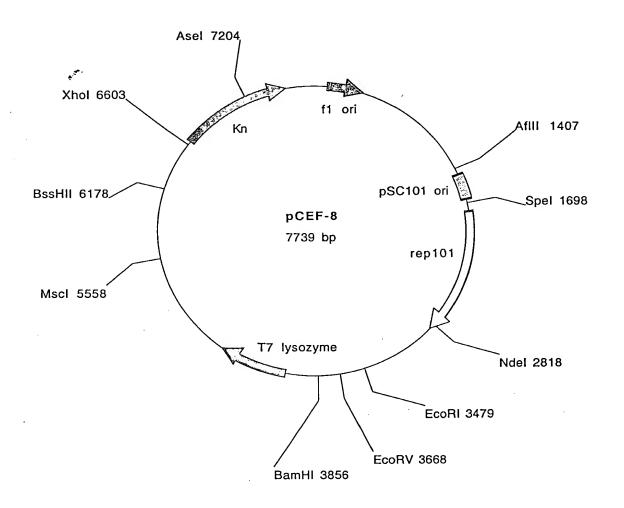
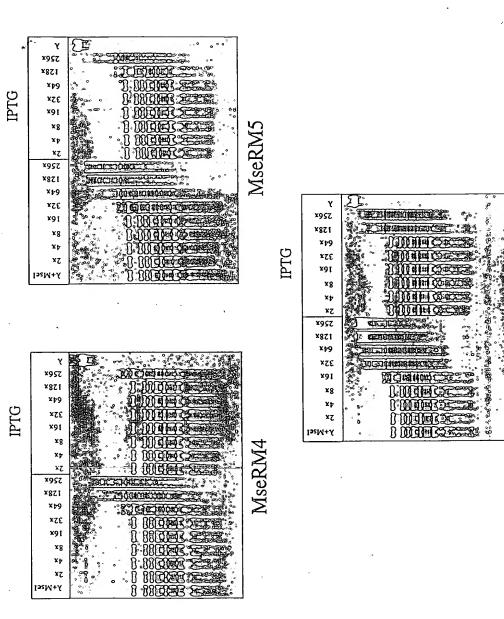


Fig- 13.



MseRM6

Fig. 14.

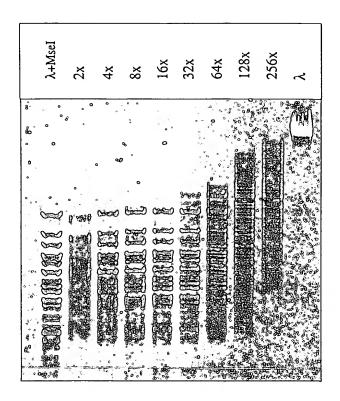


Fig.15.